

Supporting Information

Genetic variation for adaptive traits is associated with polymorphic inversions in *Littorina saxatilis*

E. L. Koch¹, H. E. Morales^{2,7}, J. Larsson¹, A. M. Westram^{1,3}, R. Faria^{1,4}, A. R. Lemmon⁵, E. M. Lemmon⁶, K. Johannesson⁷*, R. K. Butlin^{1,7*}

1 Department of Animal and Plant Sciences, University of Sheffield, Sheffield, UK

2 Evolutionary Genetics Section, Globe Institute, University of Copenhagen, Copenhagen, Denmark

3 IST Austria, Klosterneuburg, Austria

4 CIBIO-InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal

5 Department of Scientific Computing, Florida State University, Tallahassee, Florida

6 Department of Biological Science, Florida State University, Tallahassee, Florida

7 Department of Marine Sciences, University of Gothenburg, Strömstad, Sweden

* These authors contributed equally to this work.

Correspondence: e.koch@sheffield.ac.uk

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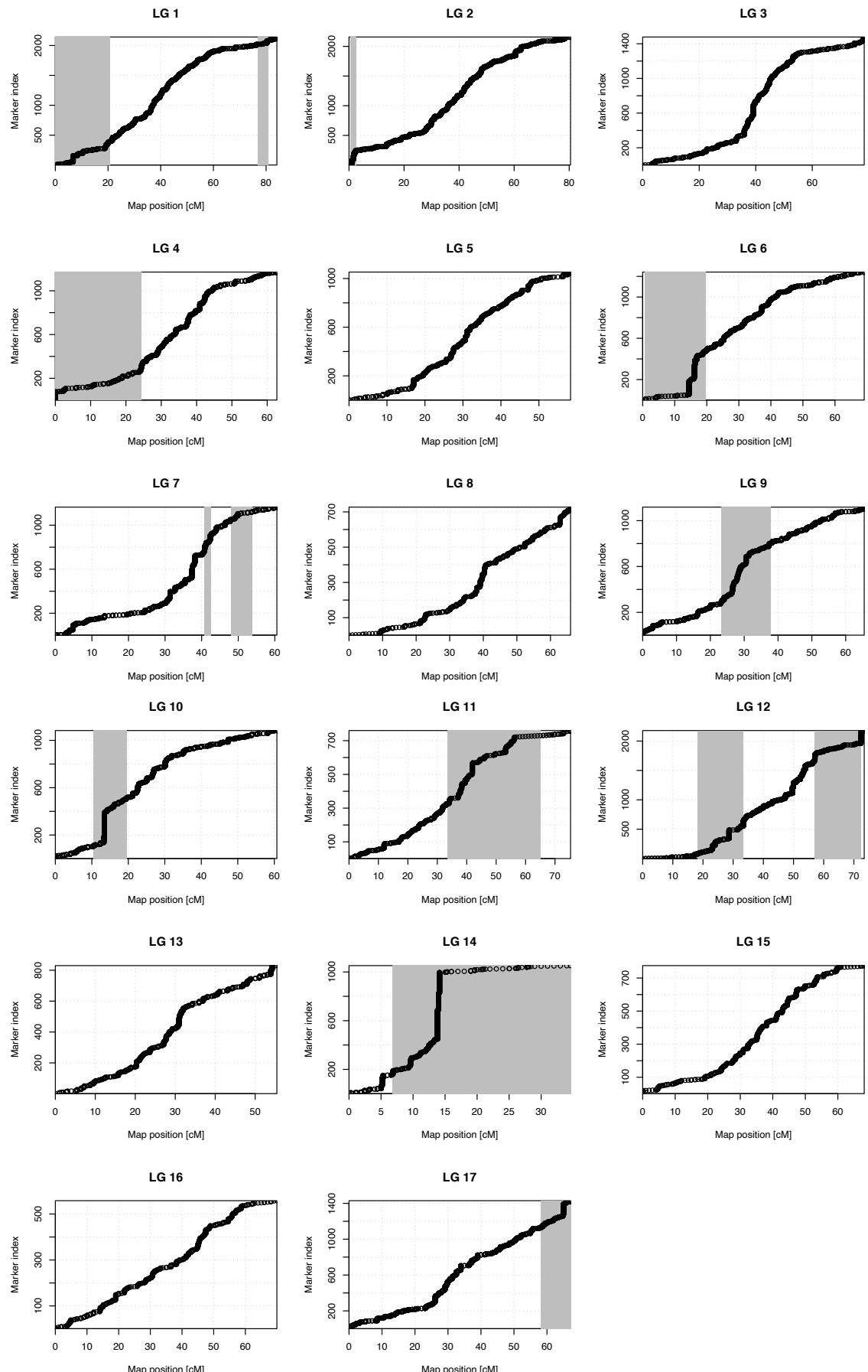


Figure S1: Mapping positions of markers for each linkage group (LG) with position on the x-axis and marker index on the y-axis. Grey background indicates the regions of putative inversion based on Faria et al. 2019, Table 1 (doi:10.1111/mec.14972). The positions in our map are based on markers that are in common with the previous linkage map. The exact positions of the inverted regions can thus only be approximated since markers at the utmost boundaries of the inversions were not always present in our data set (see Table S1). Regions of reduced recombination are visible by many markers that share the same map position and are often within the inverted regions.

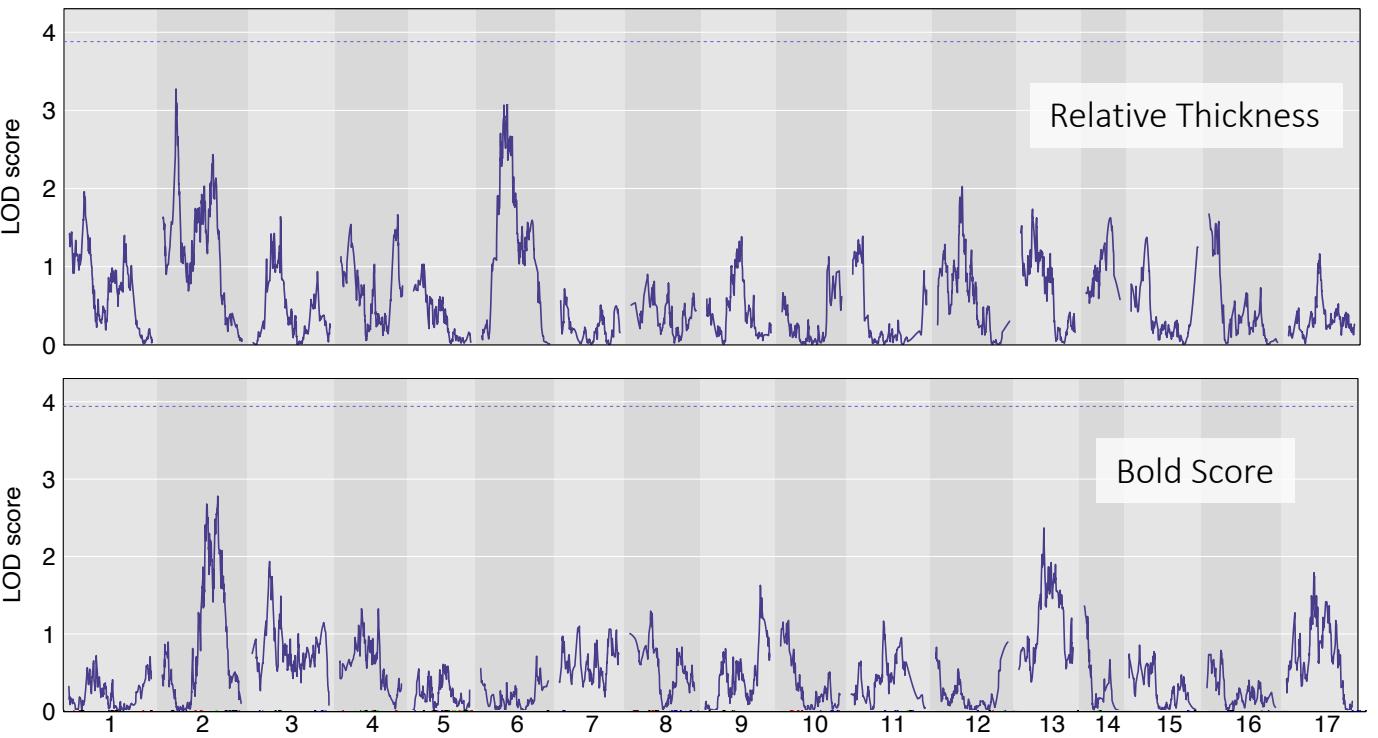


Figure S2: QTL scans for relative shell thickness (size independent) and Bold Score (time until emergence after disturbance). Dashed lines indicate genome-wide significant thresholds ($P = 0.05$)

heritability \pm SE

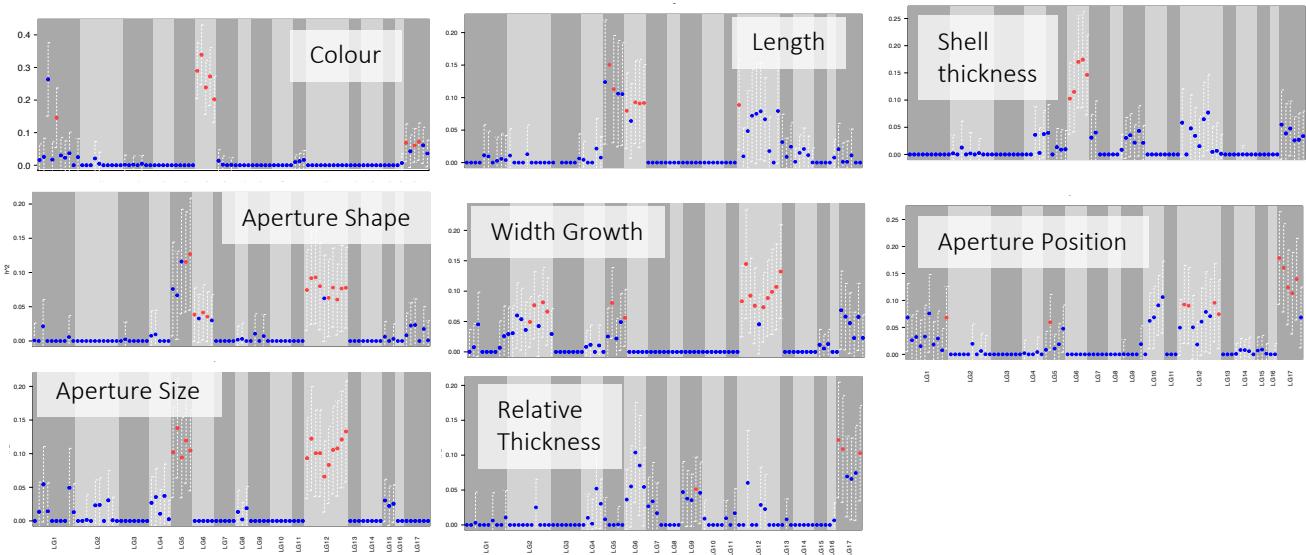
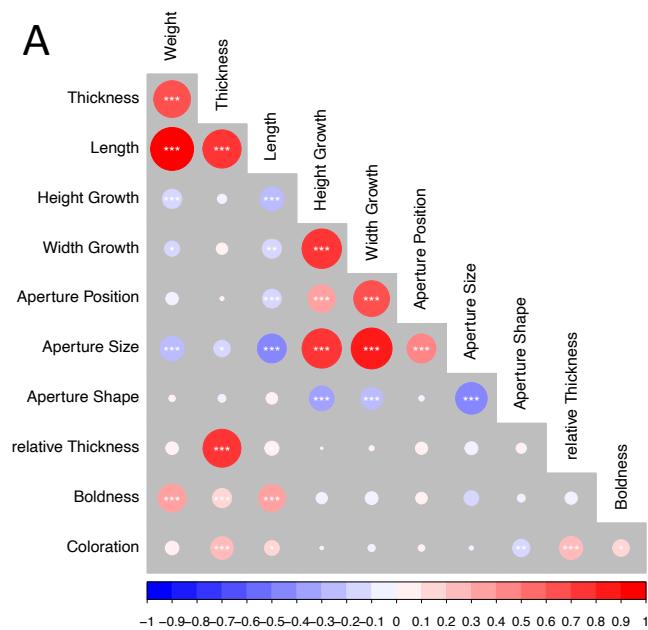
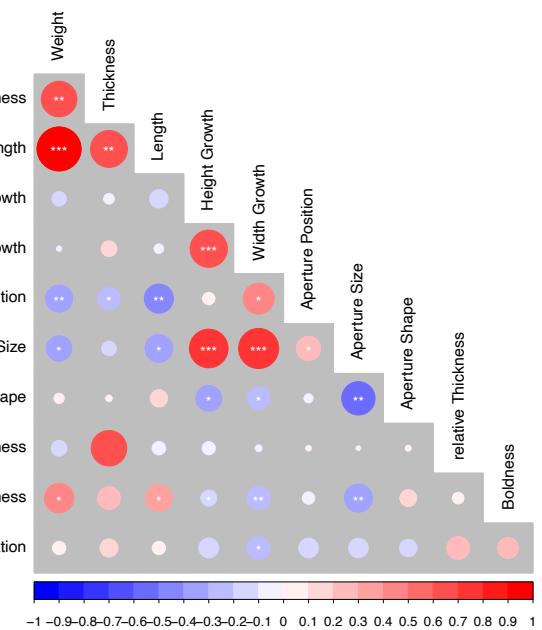
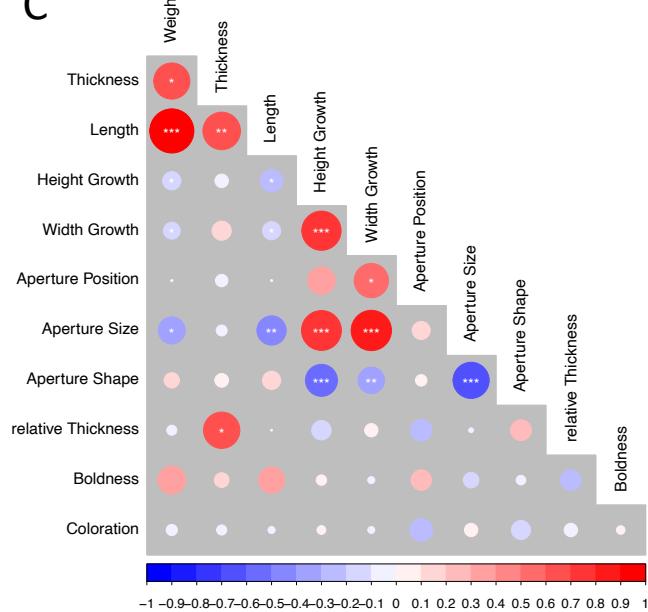
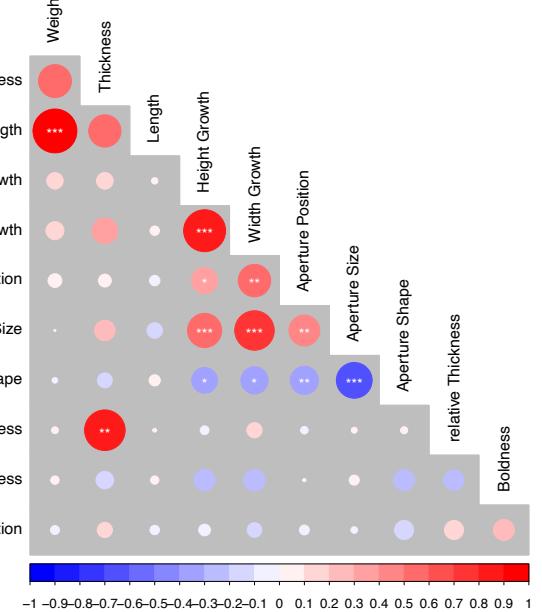
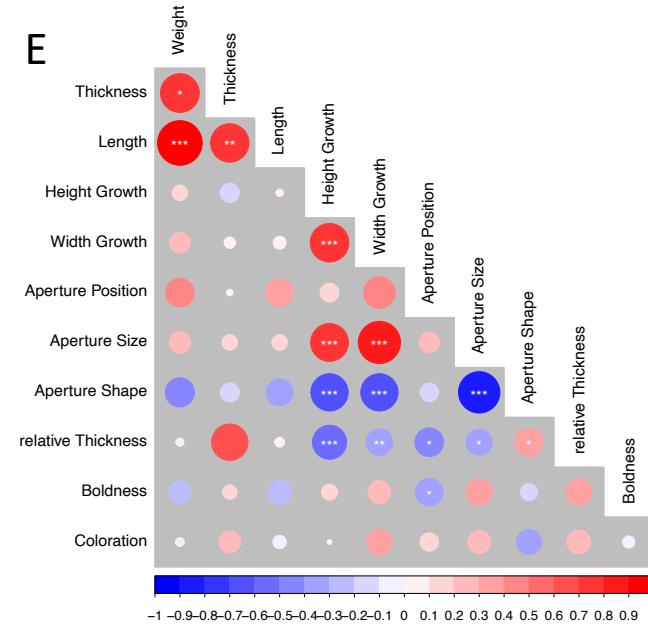
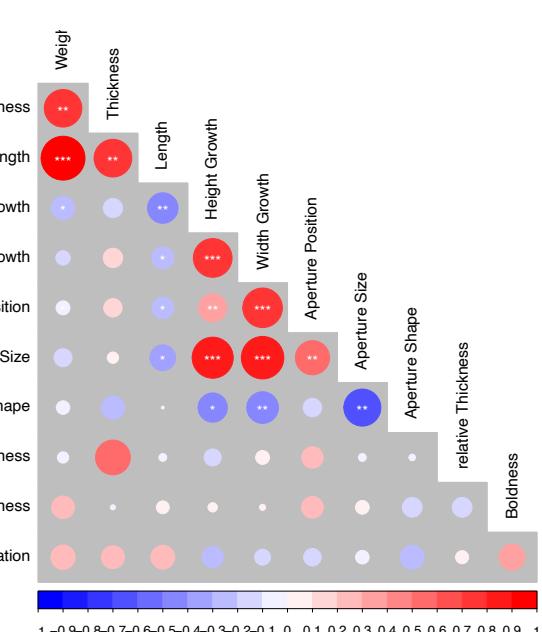
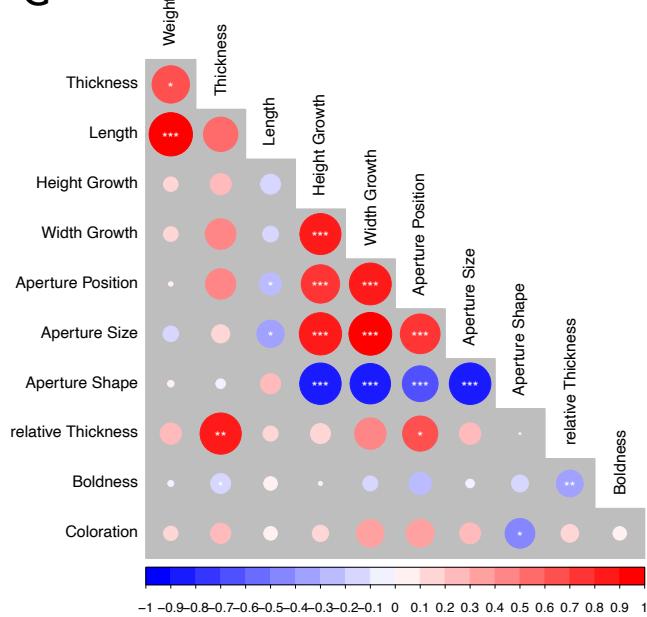


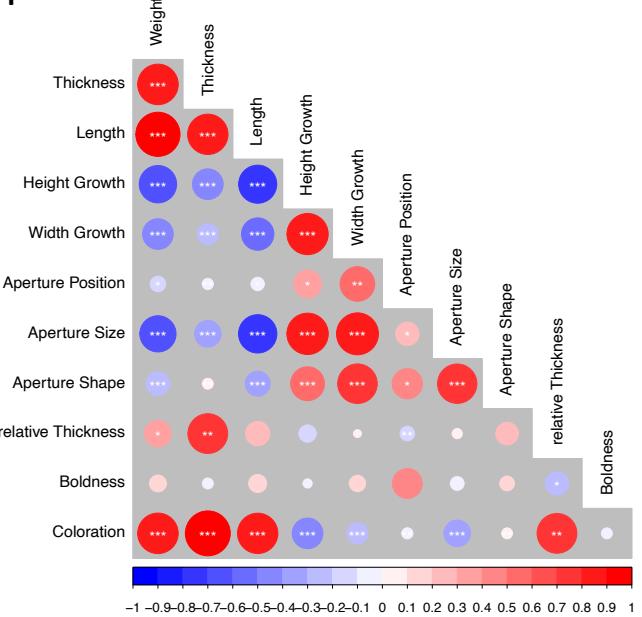
Figure S3: Regional heritability for colour, shell length, thickness, Aperture Shape, Width Growth, Aperture Position, Aperture Size, relative thickness. Each region consisted of 200 adjacent markers. Significant estimates are shown in red.

A**B****C****D****E****F**

G



H



J

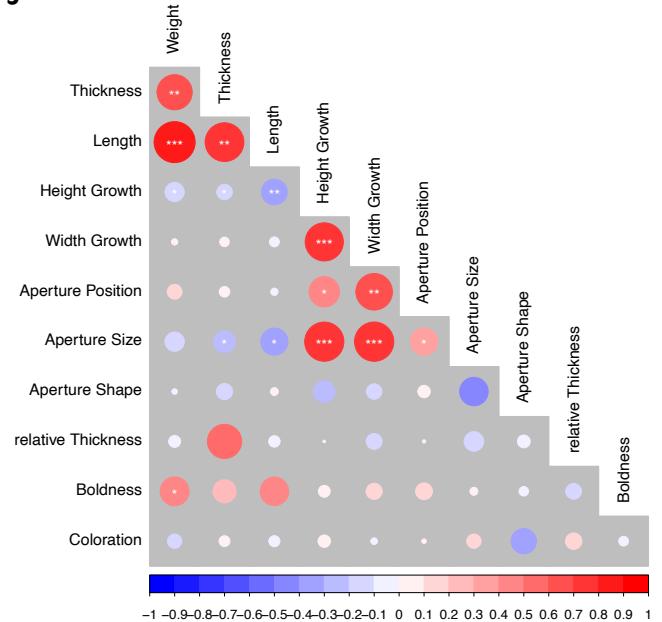
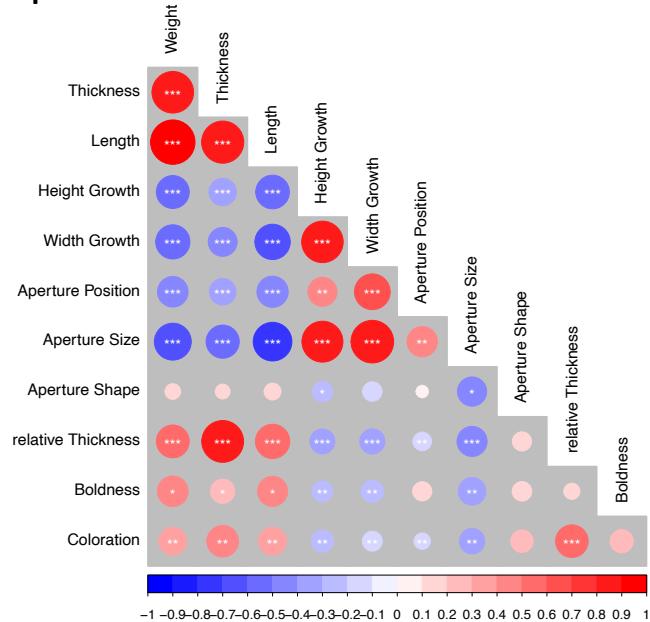
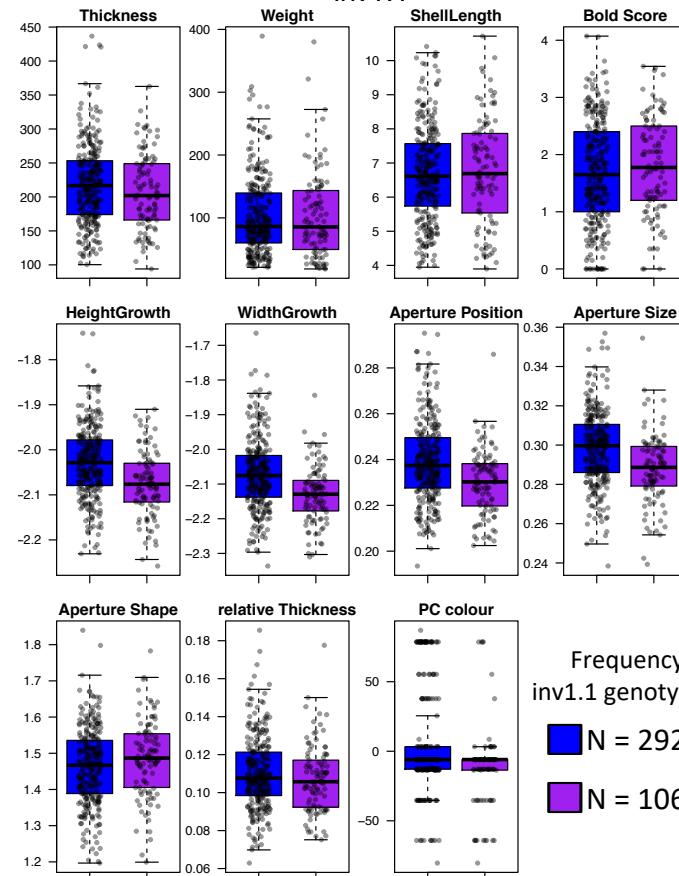


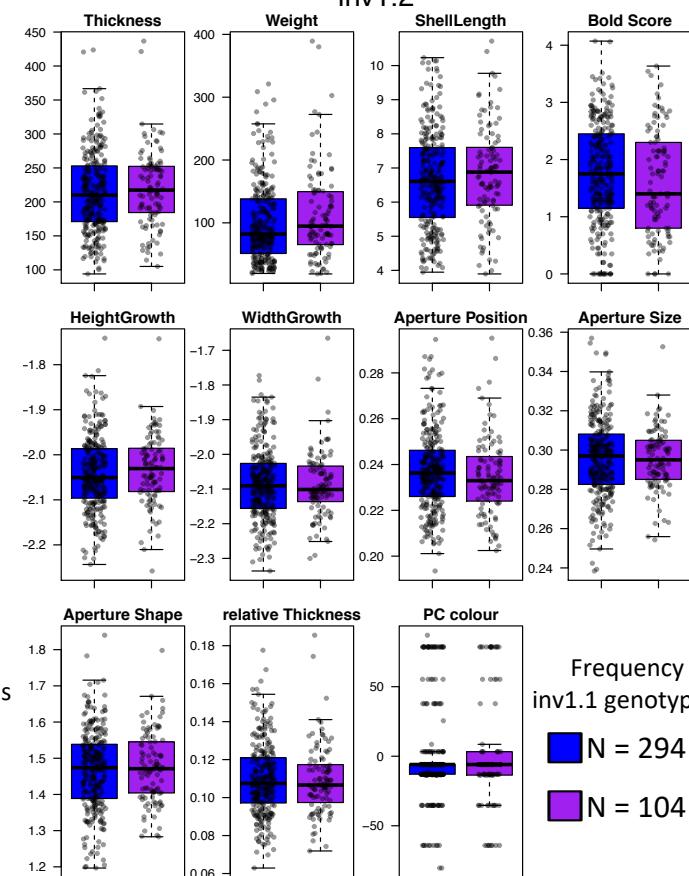
Figure S4: Phenotypic correlations between traits for all individuals (**A**) and separately for each family (**B-J**). Circles are proportional to correlation coefficients. Significance: * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$. **A:** all F2 individuals; **B:** family 81.1; **C:** family 82.1; **D:** family 83.1; **E:** family 83.2; **F:** family 91.1; **G:** family 91.2; **H:** family 92.1; **I:** family 92.2; **J:** family 93. Information for the different families can be found in the appendix.

A

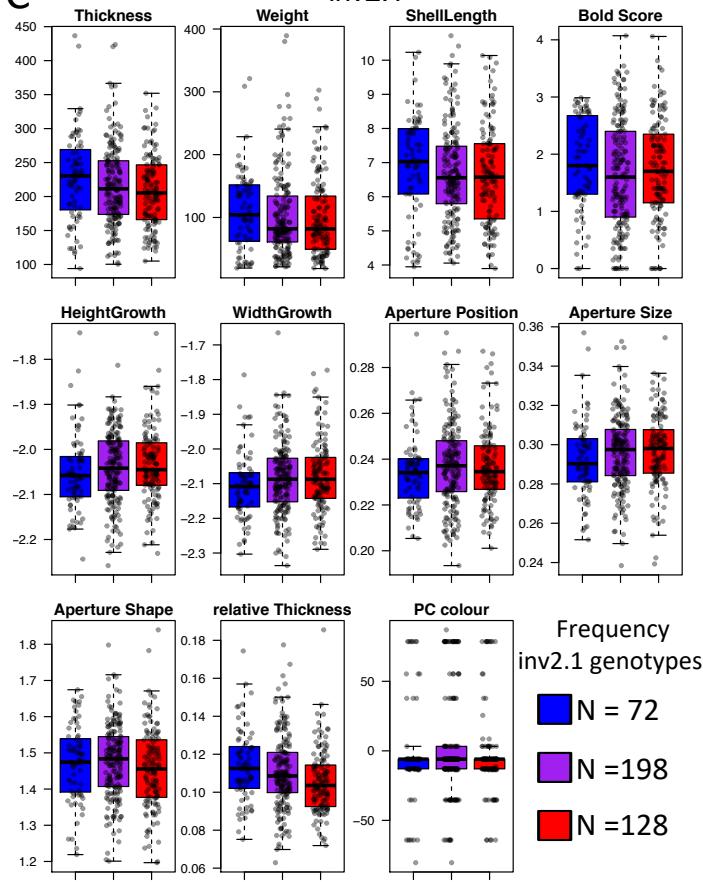
inv1.1

**B**

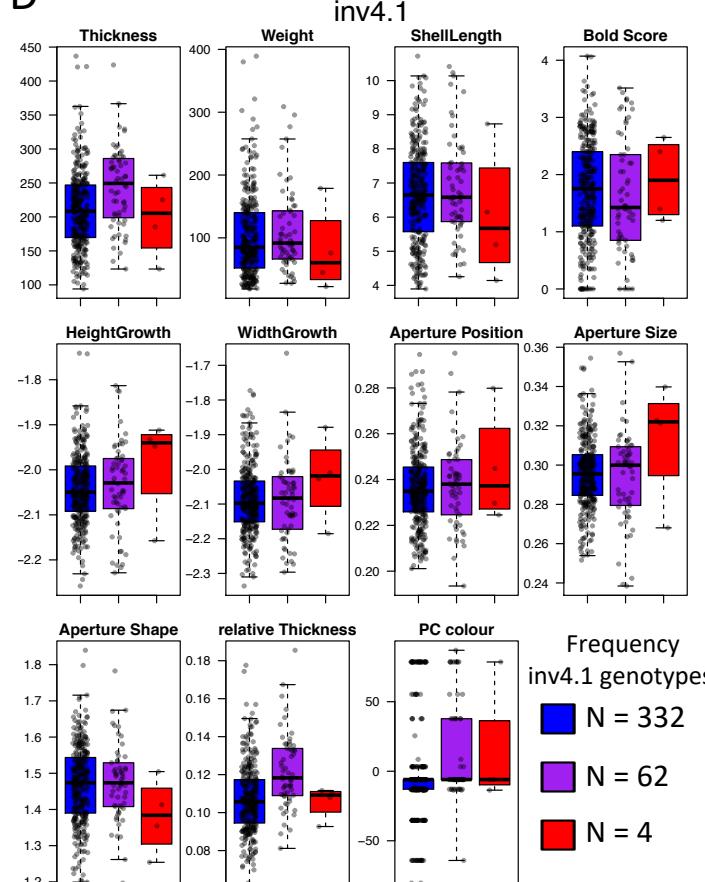
inv1.2

**C**

inv2.1

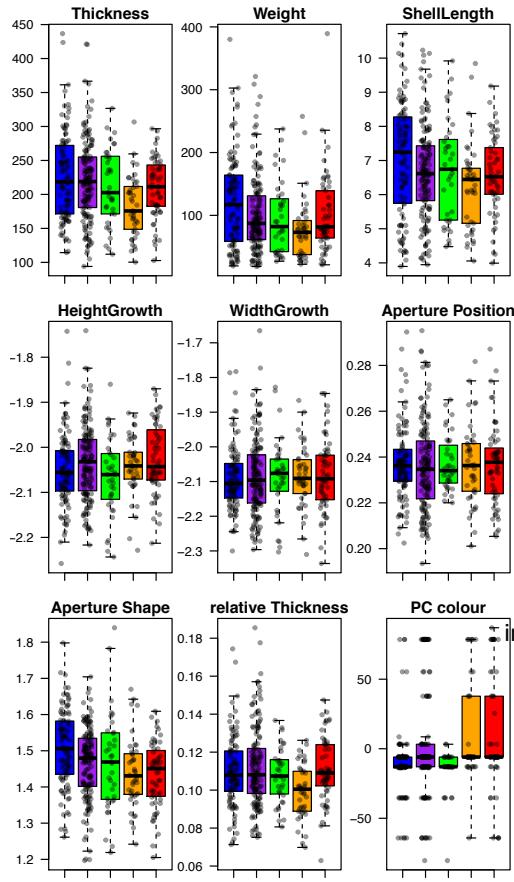
**D**

inv4.1

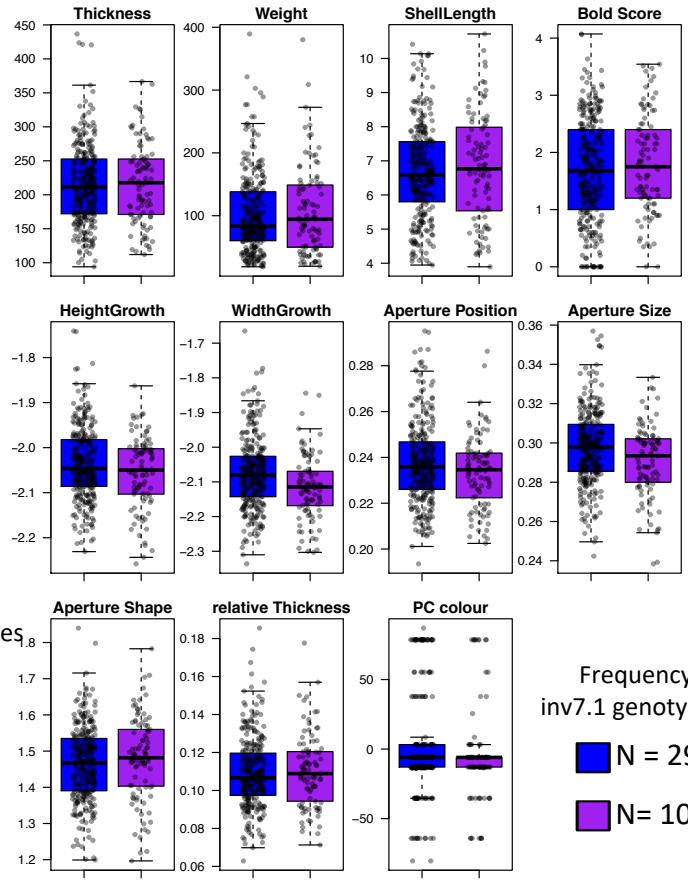
**homozygous RR****homozygous AA****heterozygous RA**

E

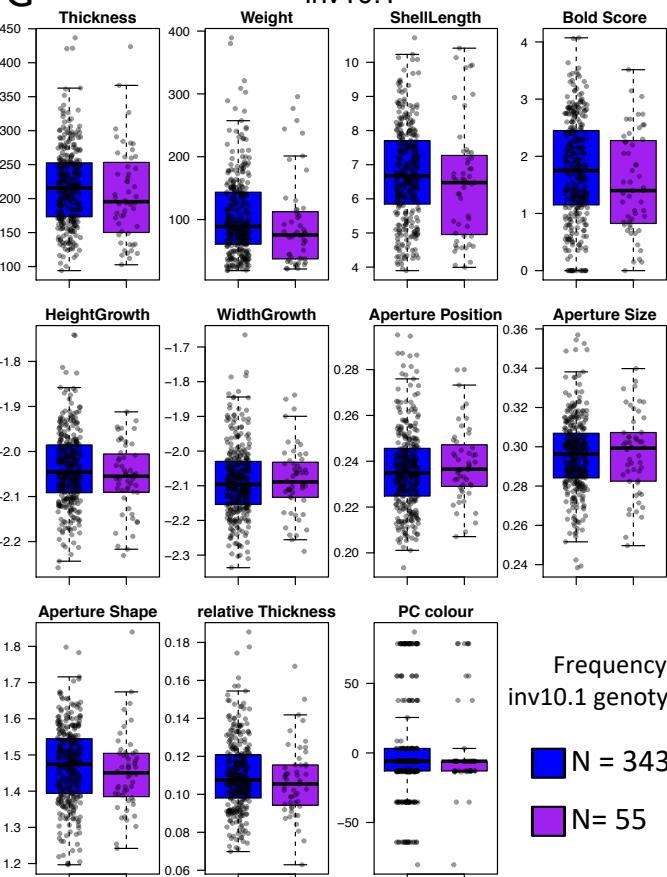
inv6.1/2

**F**

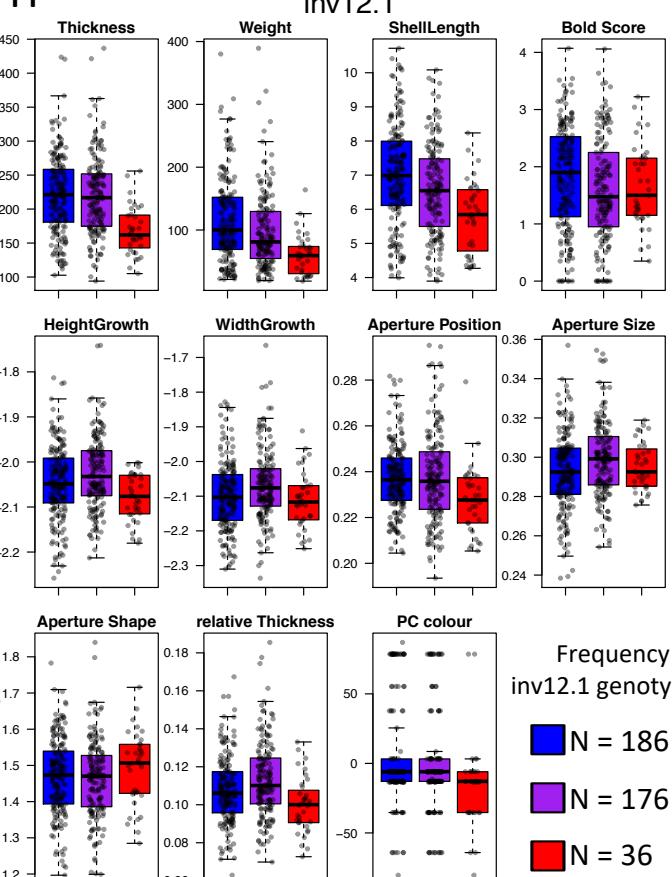
inv7.1

**G**

inv10.1

**H**

inv12.1



homozygous RR

homozygous AA

heterozygous RA

heterozygous AB

heterozygous RB

